

MAY. 1. 2002 5:38PM

TTC PALO ALTO AA alignment.txt

NO. 1073 P. 30

K

DIALIGN 2.1

Developed by Burkhard Morgenstern, Said Abdeddai
m, Kornelie Frech,
Klaus Hahn, Thomas Werner, Jens Stoye, Andreas D
ress

e-mail: burkhard.morgenstern@rp-rorer.co.uk

Published research assisted by DIALIGN 2 should
cite:

B. Morgenstern (1999),
"DIALIGN 2: improvement of the segment-to-segm
ent
approach to multiple sequence alignment."
Bioinformatics 15, 203 - 210.

Options:

=====

- 1) proteine sequences aligned
- 2) 5 "*" characters for regions of maximum similarity

Aligned sequences:

=====

length:

=====

1)	855444	501
2)	2	501

Average sequence length: 501.000

Please note that only upper-case letters are considered to
be aligned.

For more information, have a look at the user guide

http://bibiserv.techfak.uni-bielefeld.de/dialign/user_gu

[illegible]

★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★
★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★
★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★
★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★
★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★
★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★	★★★★★★★★★★

855444 101
E LGTDLVSIPH
2 101
E LGTDLVSIPH

VGAAPHPFLH RYYQRQLSST YRDLRKGVYE PYTQGKWE
VGAAPHPFLH RYYQRQLSST YRDLRKGVYV PYTQGKWE

* *****
* *****
* *****
* *****
* *****
* *****

855444 151
P DDSLEPFFDS
2 151
P DDSLEPFFDS

GPNVTVRANI AAITESDKFF INGSNWEGIL GLAYAEIAR
GPNVTVRANI AAITESDKFF INGSNWEGIL GLAYAEIAR

* *****
* *****
* *****
* *****
* *****
* *****

855444 201
I DHSLYTGSLW
2 201
I DHSLYTGSLW

LVKQTHVPNL FSLQLCGAGF PLNQSEVLAS VGGSMIIGG
LVKQTHVPNL FSLQLCGAGF PLNQSEVLAS VGGSMIIGG

* *****
* *****

* *****

* *****

* *****

855444 251
S GTTNLRLPKK
2 251
S GTTNLRLPKK

YTPIRREWYY EVIIVRVEIN GQDLKMDCKE YNYDKSIVD
YTPIRREWYY EVIIVRVEIN GQDLKMDCKE YNYDKSIVD

* *****

* *****

* *****

* *****

* *****

855444 301
I FPVISLYLMG
2 301
I FPVISLYLMG

VFEAAVKSIIK AASSTEKFPD GFWLGEQLVC WQAGTTPWN
VFEAAVKSIIK AASSTEKFPD GFWLGEQLVC WQAGTTPWN

* *****

* *****

* *****

* *****

855444 351
T GTVMGAVIME

EVTNQSFRIIT ILPOQYLRPV EDVATSQDDC YKFAISQSS

EVTNQSFRIT ILPQQYLRPV EDVATSQDDC YKFAISQSS

[illegible]

GFYVVFDRAR KRIGFAVSAC HVHDEFRTAA VEGPFVTLT
GFYVVFDRAR KRIGFAVSAC HVHDEFRTAA VEGPFVTLT

*****	*****	*****	*****
*****	*****	*****	*****
*****	*****	*****	*****
*****	*****	*****	*****
*****	*****	*****	*****

DESTLMTIAY VMAAICALFM LPLCLMVCQW RCLRCLRQQ
DESTLMTIAY VMAAICALFM LPLCLMVCQW RCLRCLRQQ

* ****

* ****

855444

2

K

K

*

*

*

*

*

Alignment (FASTA format):

=====

>855444

MAQALPWLLLWMGAGVLP AHGTQH GIRLPLRSGLGGAPLGLRLPRETDEE
PEEPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFA
VGAAPHFPLHRYYQRLSSTYRDLRKGVYEPYTOGKWEDELGTDLVSI PH
GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYVEV IIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR LPKK
VFEEAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNI FPVISLYLMG
EVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQT
DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDFADDISLL
K

>2

MAQALPWLLLWMGAGVLP AHGTQH GIRLPLRSGLGGAPLGLRLPRETDEE
PEEPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFA
VGAAPHFPLHRYYQRLSSTYRDLRKGVYVPTOGKWEDELGTDLVSI PH
GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYVEV IIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLR LPKK
VFEEAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNI FPVISLYLMG
EVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQT
DESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDFADDISLL